This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: TITLE, AUTHORS, etc

Code assigned:	***2013.025a-dB***	(to be completed by ICTV officers)

Short title: To create a new genus, the *Phicbklikevirus*, within the family *Siphoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☒	

Author(s) with e-mail address(es) of the proposer:

Evelien Adriaenssens Evelien.Adriaenssens@gmail.com
Andrew M. Kropinski akropins@uoguelph.ca
Rob Lavigne rob.lavigne@biw.kuleuven.be

List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:	June 2013
Date of this revision (if different to above):	July 2014

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	*2013.025aB*	(assigned by ICTV officers)

To create 5 new species within:

Genus:	***Phicbklikevirus* (new)**
Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

	GenBank sequence accession number(s) of reference isolate:
Caulobacter phage phicbk	JX100813
Caulobacter phage magneto	JX100812
Caulobacter phage swift	JX100809
Caulobacter phage karma	JX100811
Caulobacter phage rogue	JX100814

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

BLASTN analyses reveal that these five *Caulobacter* phages are related and distinct from any other phage. We have chosen 95% DNA sequence identity as the criterion for demarcation of species.

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2013.025bB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Siphoviridae***
Order:	***Caudovirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2013.025cB***	(assigned by ICTV officers)

To name the new genus: *Phicbklikevirus*

Assigning the type species and other species to a new genus

Code	***2013.025dB***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Caulobacter phage phicbk	Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

5

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

Origin of the new genus name:

Caulobacter phage phiCbK

Reasons to justify the choice of type species:

The original isolate of this group.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

The *Phicbklikevirus* members possess large (205-213 kb) genomes with approximately 10kb terminal repeats (1). The capsids are prolate measuring 205-213nm in length by 56-63nm in diameter. The tails measure 293-319nm. "Phage phiCbK and related phages have been shown to have a unique filamentous structure emanating from the top vertex of the capsid. This head filament was found to mediate primary attachment of the virion to the flagellum and thus more efficient adsorption to the swarmer cell" (2).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1: Gill JJ, Berry JD, Russell WK, Lessor L, Escobar Garcia DA, Hernandez D, Kane A, Keene J, Maddox M, Martin R, Mohan S, Thorn AM, Russell DH, Young R. 2012. The Caulobacter crescentus phage phiCbK: genomics of a canonical phage. BMC Genomics. 13(1):542.

2: Panis G, Lambert C, Viollier PH. 2012. Complete genome sequence of Caulobacter crescentus bacteriophage phiCbK. J Virol. 86(18):10234-5.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Table 1. Phage genomes

Phage	**Accession No.**	**Size (bp)**	**Terminal Repeats (bp)**	**Mol%G+C**	**tRNAs**	**% DNA sequence relatedness**	**% Protein relatedness**
Caulobacter phage phiCbK	JX100813	205,423	10,287	66.2	26	100%	100%
Caulobacter phage CcrMagneto	JX100812	208,983	9,946	66.6	27	92.0	97.8
Caulobacter phage CcrSwift	JX100809	209,245	9,971	66.1	27	89.8	95.3
Caulobacter phage CcrKarma	JX100811	211,574	10,254	66.2	26	91.9	98.7
Caulobacter phage CcrRogue	JX100814	213,399	10,321	66.6	23	ND	81.8

(a) Calculated with EMBOSS Stretcher (relative to Phicbk)
(b) Calculated with CoreGenes 2.0

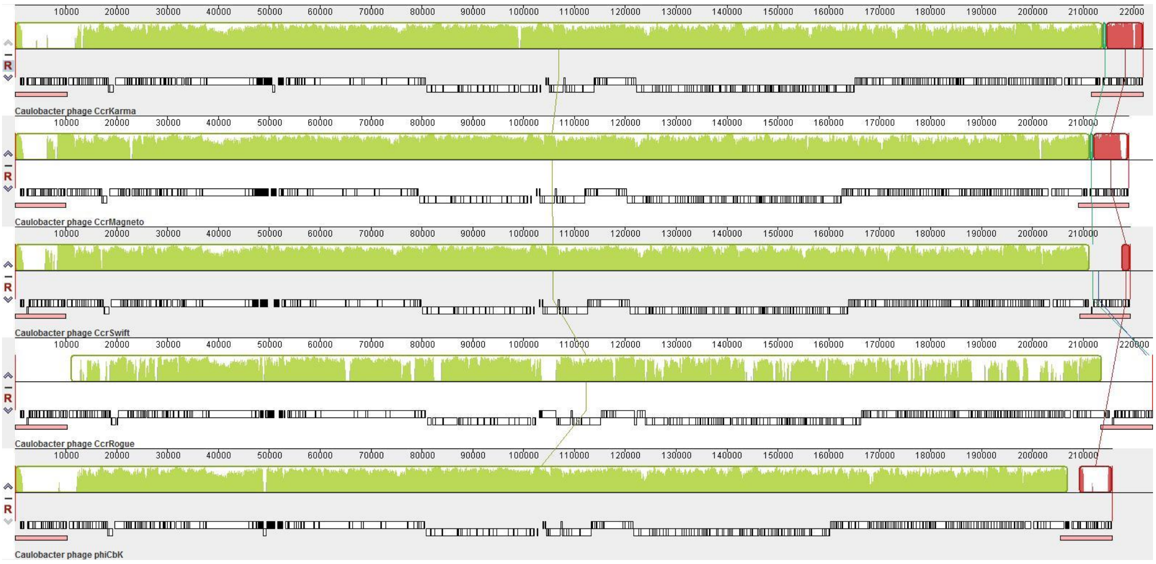

Figure 1. progressiveMauve alignment of the genomes of the these *Caulobacter* phages indicates that they are very similar.

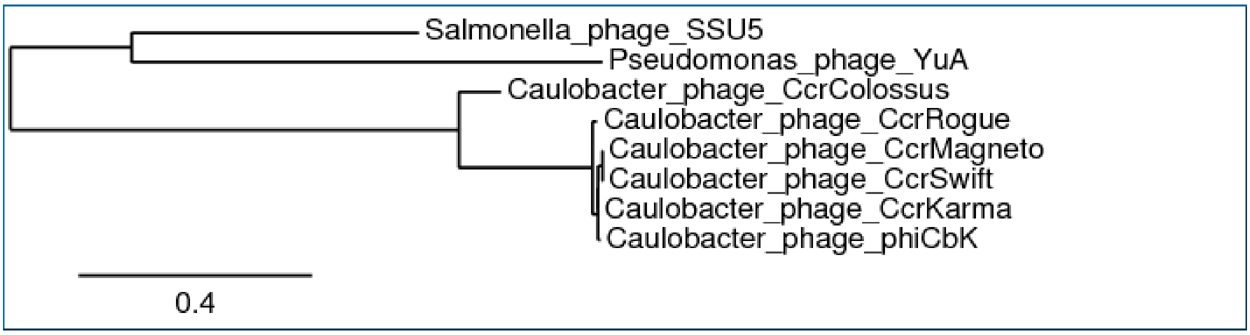

Figure 2. Phylogenetic analysis of the major capsid protein using “one click” phylogeny.fr. The outlier, Pseudomonas phage YuA belongs to the *Yualikevirus*.